

SEQUENCE LISTING

(1) GENERAL INFORMATION:

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(i) APPLICANT: John J. Castellot, Jr.

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(ii) TITLE OF INVENTION: Novel Heparin-Induced CCN-Like Molecules  
and Uses Therefor

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

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(A) ADDRESSEE: LAHIVE & COCKFIELD, LLP  
(B) STREET: 28 State Street  
(C) CITY: Boston  
(D) STATE: Massachusetts  
(E) COUNTRY: USA  
(F) ZIP: 02109

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(v) COMPUTER READABLE FORM:

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(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

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(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

35

(A) APPLICATION NUMBER:  
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

40

(A) NAME: Amy E. Mandragouras  
(B) REGISTRATION NUMBER: 36,207  
(C) REFERENCE/DOCKET NUMBER: MBI-004

(ix) TELECOMMUNICATION INFORMATION:

45

(A) TELEPHONE: (617)227-7400  
(B) TELEFAX: (617)742-4214

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 1708 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 249..1001

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

	GACGCTTCTG ATCTCCAGAG GACCCTGGGG TGGGACAGGG GCCTTGGCAA GGCTGCAGCC	60
	GCTGGGCAGT GGCTTGAAT GGAGGTCTTT ATTACTGGGA ACTGAGGAGC TAAGAGGCTC	120
10	CTGTCACTT GTCCTAAAGT CTTAGCACTT GTGGTGGCTT GGGCTTCACA CACTGTCAGA	180
	CACCTTCGTG GTGGCCTCCA CGGCCTCACC TTCAGGTTTG AAGCTGGCTC CACAAGGGAC	240
15	ACGGTGAC ATG AGG GGC AGC CCA CTG ATC CAT CTT CTG GCC ACT TCC TTC	290
	Met Arg Gly Ser Pro Leu Ile His Leu Leu Ala Thr Ser Phe	
	1 5 10	
	CTC TGC CTT CTC TCA ATG GTG TGT GCC CAG CTG TGC CGG ACA CCC TGT	338
20	Leu Cys Leu Leu Ser Met Val Cys Ala Gln Leu Cys Arg Thr Pro Cys	
	15 20 25 30	
	ACC TGT CCT TGG ACA CCA CCC CAG TGC CCA CAG GGG GTA CCC CTG GTG	386
25	Thr Cys Pro Trp Thr Pro Pro Gln Cys Pro Gln Gly Val Pro Leu Val	
	35 40 45	
	CTG GAT GGC TGT GGC TGC TGT AAA GTG TGT GCA CGG AGG CTG GGG GAG	434
	Leu Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Arg Arg Leu Gly Glu	
	50 55 60	
30	TCC TGC GAC CAC CTG CAT GTC TGC GAC CCC AGC CAG GGC CTG GTT TGT	482
	Ser Cys Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu Val Cys	
	65 70 75	
35	CAG CCT GGG GCA GGC CCT GGC GGC CAT GGG GCT GTG TGT CTC TTG GAT	530
	Gln Pro Gly Ala Gly Pro Gly Gly His Gly Ala Val Cys Leu Leu Asp	
	80 85 90	
	GAG GAT GAC GGT AGC TGT GAG GTG AAT GGC CGC AGG TAC CTG GAT GGA	578
40	Glu Asp Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu Asp Gly	
	95 100 105 110	
	GAG ACC TTT AAA CCC AAT TGC AGG GTC CTG TGC CGC TGT GAT GAC GGT	626
45	Glu Thr Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp Asp Gly	
	115 120 125	
	GGC TTC ACC TGC CTG CCG CTG TGC AGT GAG GAT GTG CGG CTG CCC AGC	674
	Gly Phe Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser	
	130 135 140	
50	TGG GAC TGC CCA CGC CCC AAG AGA ATA CAG GTG CCA GGA AAG TGC TGC	722
	Trp Asp Cys Pro Arg Pro Lys Arg Ile Gln Val Pro Gly Lys Cys Cys	
	145 150 155	
55	CCC GAG TGG GTA TGT GAC CAG GGA GTG ACA CCG GCG ATC CAG CGC TCC	770
	Pro Glu Trp Val Cys Asp Gln Gly Val Thr Pro Ala Ile Gln Arg Ser	
	160 165 170	

1001004001

	ACG GCG CAA GGA CAC CAA CTT TCT GCC CTT GTC ACT CCT GCC TCT GCT	818
	Thr Ala Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro Ala Ser Ala	
	175 180 185 190	
5	GAT GCT CCT TGT CCA AAT TGG AGC ACA GCC TGG GGC CCC TGC TCA ACC	866
	Asp Ala Pro Cys Pro Asn Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr	
	195 200 205	
10	ACC TGT GGG CTG GGC ATA GCC ACC CGA GTG TCC AAC CAG AAC CGA TTC	914
	Thr Cys Gly Leu Gly Ile Ala Thr Arg Val Ser Asn Gln Asn Arg Phe	
	210 215 220	
15	TGC CAA CTG GAG ATC CAA CGC CGC CTG TGT CTG CCC AGA CCC TGC CTG	962
	Cys Gln Leu Glu Ile Gln Arg Arg Leu Cys Leu Pro Arg Pro Cys Leu	
	225 230 235	
20	GCA GCC AGG AGC CAC AGC TCA TGG AAC AGT GCT TTC TAAGGCCAAC	1008
	Ala Ala Arg Ser His Ser Ser Trp Asn Ser Ala Phe	
	240 245 250	
25	TGGGGATGCG GATACAGGGC CTGCCATCCT CAGCAAATGA CCCTAGGACC AGGCCCTGGA	1068
	CTGCTGGTAG ATGCTCTTCT CCATGCTCTT GGCTGCAGTT AACTGTCCTG CTTGGATTCA	1128
	CTGTGTAGAG CCACTGAGCG ATCCCTGCTC TGTCTGAGGT AGGCGGAGCA GGTGACCAGC	1188
	TCCAGTTCTC TGGTTCAGCC TGGAAATTCTG GGTTCCTCTG GCTCATTCCT CAAAACATCC	1248
30	CTGTACAAAA AGGACAACCA AAAAGACCTT TAAACCTAGG CTATACTGGG CAAACCTGGC	1308
	CACCGTGCTG GGGATAAGGT CAATGTTAGG ACCAGACAGC AGATTGCCTG AACTTCCAA	1368
35	TTCCCTTCTT GGACTTCTGT ATGCTTGTCC CCAAAGATGA TGAATGAACT CGTAAGTGTA	1428
	CCTTCCCTGA CCTGAGAACA CCCTGCCTGC TCGGGAAGTA TTCAGGGGCA GAATTCTCTG	1488
	TGAACATGAA GAGATGAATC AACTGTCTCT TAAGAAATTC CTGAAAGTCC AGGAACTTGA	1548
40	GCTTTGTATT TTCAGGAATG CACATCTCTT AAGCACTCGC AAAACAGGAA GGCTCCACAC	1608
	CTCTGGCAGG CCAGGGCCTT TCTCTTCAGC ATGAGAAAGA CAAGGGACAG CAGAGTACTC	1668
45	TCCTCTGGAG GACTAGTCTA GCCTAGAATA AACACCCAAA	1708

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Arg Gly Ser Pro Leu Ile His Leu Leu Ala Thr Ser Phe Leu Cys  
1 5 10 15

Leu Leu Ser Met Val Cys Ala Gln Leu Cys Arg Thr Pro Cys Thr Cys  
5 20 25 30

Pro Trp Thr Pro Pro Gln Cys Pro Gln Gly Val Pro Leu Val Leu Asp  
35 40 45

Gly Cys Gly Cys Cys Lys Val Cys Ala Arg Arg Leu Gly Glu Ser Cys  
10 50 55 60

Asp His Leu His Val Cys Asp Pro Ser Gln Gly Leu Val Cys Gln Pro  
15 65 70 75 80

Gly Ala Gly Pro Gly Gly His Gly Ala Val Cys Leu Leu Asp Glu Asp  
85 90 95

Asp Gly Ser Cys Glu Val Asn Gly Arg Arg Tyr Leu Asp Gly Glu Thr  
20 100 105 110

Phe Lys Pro Asn Cys Arg Val Leu Cys Arg Cys Asp Asp Gly Gly Phe  
115 120 125

Thr Cys Leu Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp  
25 130 135 140

Cys Pro Arg Pro Lys Arg Ile Gln Val Pro Gly Lys Cys Cys Pro Glu  
30 145 150 155 160

Trp Val Cys Asp Gln Gly Val Thr Pro Ala Ile Gln Arg Ser Thr Ala  
165 170 175

Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro Ala Ser Ala Asp Ala  
35 180 185 190

Pro Cys Pro Asn Trp Ser Thr Ala Trp Gly Pro Cys Ser Thr Thr Cys  
195 200 205

Gly Leu Gly Ile Ala Thr Arg Val Ser Asn Gln Asn Arg Phe Cys Gln  
40 210 215 220

Leu Glu Ile Gln Arg Arg Leu Cys Leu Pro Arg Pro Cys Leu Ala Ala  
45 225 230 235 240

Arg Ser His Ser Ser Trp Asn Ser Ala Phe  
245 250

(2) INFORMATION FOR SEQ ID NO:3:

- 50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 753 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: cDNA

(A) NAME/KEY: CDS

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CAA GGA CAC CAA CTT TCT GCC CTT GTC ACT CCT GCC TCT GCT GAT GCT 576  
Gln Gly His Gln Leu Ser Ala Leu Val Thr Pro Ala Ser Ala Asp Ala  
180 185 190

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(2) INFORMATION FOR SEQ ID NO:4:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide  
(v) FRAGMENT TYPE: internal

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:  
  
Gly Cys Gly Cys Cys Xaa Xaa Cys  
1 5

35 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: cDNA

45 (ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..177

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:  
  
TGT GAG GTG AAT GGC CGC AGG TAC CTG GAT GGA GAG ACC TTT AAA CCC  
55 Cys Glu Val Asn Gly Arg Arg Tyr Leu Asp Gly Glu Thr Phe Lys Pro  
1 5 10 15

5 CCG CTG TGC AGT GAG GAT GTG CGG CTG CCC AGC TGG GAC TGC CCA CGC 144  
Pro Leu Cys Ser Glu Asp Val Arg Leu Pro Ser Trp Asp Cys Pro Arg  
35 40 45

10 CCC AAG AGA ATA CAG GTG CCA GGA AAG TGC TGC 177  
Pro Lys Arg Ile Gln Val Pro Gly Lys Cys Cys  
50 55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asn Cys Arg Val Leu Cys Arg Cys Asp Asp Gly Gly Phe Thr Cys Leu  
20 25 30

35           Pro Lys Arg Ile Gln Val Pro Gly Lys Cys Cys  
              50                               55

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Trp Xaa Xaa Cys Ser Xaa Xaa Cys Gly Xaa Gly Xaa Xaa Thr Arg  
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

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- (A) NAME/KEY: CDS
- (B) LOCATION: 1..210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

15

CAG	CTG	TGC	CGG	ACA	CCC	TGT	ACC	TGT	CCT	TGG	ACA	CCA	CCC	CAG	TGC	48
Gln	Leu	Cys	Arg	Thr	Pro	Cys	Thr	Cys	Pro	Trp	Thr	Pro	Pro	Gln	Cys	
1				5					10					15		

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CCA	CAG	GGG	GTA	CCC	CTG	GTG	CTG	GAT	GGC	TGT	GGC	TGC	TGT	AAA	GTG	96
Pro	Gln	Gly	Val	Pro	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	
			20					25						30		

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TGT	GCA	CGG	AGG	CTG	GGG	GAG	TCC	TGC	GAC	CAC	CTG	CAT	GTC	TGC	GAC	144
Cys	Ala	Arg	Arg	Leu	Gly	Glu	Ser	Cys	Asp	His	Leu	His	Val	Cys	Asp	
		35					40					45				

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CCC	AGC	CAG	GGC	CTG	GTT	TGT	CAG	CCT	GGG	GCA	GGC	CCT	GGC	GGC	CAT	192
Pro	Ser	Gln	Gly	Leu	Val	Cys	Gln	Pro	Gly	Ala	Gly	Pro	Gly	Gly	His	
	50					55					60					

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GGG	GCT	GTG	TGT	CTC	TTG											210
Gly	Ala	Val	Cys	Leu	Leu											
65					70											

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

50

Gln	Leu	Cys	Arg	Thr	Pro	Cys	Thr	Cys	Pro	Trp	Thr	Pro	Pro	Gln	Cys
1				5					10					15	

Pro	Gln	Gly	Val	Pro	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val
			20					25						30	

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Cys	Ala	Arg	Arg	Leu	Gly	Glu	Ser	Cys	Asp	His	Leu	His	Val	Cys	Asp
		35					40					45			

Pro	Ser	Gln	Gly	Leu	Val	Cys	Gln	Pro	Gly	Ala	Gly	Pro	Gly	Gly	His
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"10010403" 3001001



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Gly Ala Val Cys Leu Leu  
65 70

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(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

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(A) NAME/KEY: CDS  
(B) LOCATION: 1..174

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

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CCT	TGT	CCA	AAT	TGG	AGC	ACA	GCC	TGG	GGC	CCC	TGC	TCA	ACC	ACC	TGT	48
Pro	Cys	Pro	Asn	Trp	Ser	Thr	Ala	Trp	Gly	Pro	Cys	Ser	Thr	Thr	Cys	
1				5					10					15		

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GGG	CTG	GGC	ATA	GCC	ACC	CGA	GTG	TCC	AAC	CAG	AAC	CGA	TTC	TGC	CAA	96
Gly	Leu	Gly	Ile	Ala	Thr	Arg	Val	Ser	Asn	Gln	Asn	Arg	Phe	Cys	Gln	
			20					25					30			

35

CTG	GAG	ATC	CAA	CGC	CGC	CTG	TGT	CTG	CCC	AGA	CCC	TGC	CTG	GCA	GCC	144
Leu	Glu	Ile	Gln	Arg	Arg	Leu	Cys	Leu	Pro	Arg	Pro	Cys	Leu	Ala	Ala	
		35				40						45				

40

AGG	AGC	CAC	AGC	TCA	TGG	AAC	AGT	GCT	TTC							174
Arg	Ser	His	Ser	Ser	Trp	Asn	Ser	Ala	Phe							
		50				55										

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 58 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

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Pro	Cys	Pro	Asn	Trp	Ser	Thr	Ala	Trp	Gly	Pro	Cys	Ser	Thr	Thr	Cys	
1				5					10					15		
Gly	Leu	Gly	Ile	Ala	Thr	Arg	Val	Ser	Asn	Gln	Asn	Arg	Phe	Cys	Gln	
			20					25					30			

5            Arg Ser His Ser Ser Trp Asn Ser Ala Phe  
                 50                            55

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 681 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

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(ix) FEATURE:
      (A) NAME/KEY: CDS
20      (B) LOCATION: 1..681

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25	CAG	CTG	TGC	CGG	ACA	CCC	TGT	ACC	TGT	CCT	TGG	ACA	CCA	CCC	CAG	TGC	48
	Gln	Leu	Cys	Arg	Thr	Pro	Cys	Thr	Cys	Pro	Trp	Thr	Pro	Pro	Gln	Cys	
	1				5					10					15		
30	CCA	CAG	GGG	GTA	CCC	CTG	GTG	CTG	GAT	GGC	TGT	GGC	TGC	TGT	AAA	GTG	96
	Pro	Gln	Gly	Val	Pro	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	Lys	Val	
				20					25					30			
35	TGT	GCA	CGG	AGG	CTG	GGG	GAG	TCC	TGC	GAC	CAC	CTG	CAT	GTC	TGC	GAC	144
	Cys	Ala	Arg	Arg	Leu	Gly	Glu	Ser	Cys	Asp	His	Leu	His	Val	Cys	Asp	
			35					40					45				
40	CCC	AGC	CAG	GGC	CTG	GTT	TGT	CAG	CCT	GGG	GCA	GGC	CCT	GGC	GGC	CAT	192
	Pro	Ser	Gln	Gly	Leu	Val	Cys	Gln	Pro	Gly	Ala	Gly	Pro	Gly	Gly	His	
		50					55					60					
45	GGG	GCT	GTG	TGT	CTC	TTG	GAT	GAG	GAT	GAC	GGT	AGC	TGT	GAG	GTG	AAT	240
	Gly	Ala	Val	Cys	Leu	Leu	Asp	Glu	Asp	Asp	Gly	Ser	Cys	Glu	Val	Asn	
	65					70				75						80	
50	GGC	CGC	AGG	TAC	CTG	GAT	GGA	GAG	ACC	TTT	AAA	CCC	AAT	TGC	AGG	GTC	288
	Gly	Arg	Arg	Tyr	Leu	Asp	Gly	Glu	Thr	Phe	Lys	Pro	Asn	Cys	Arg	Val	
					85				90						95		
55	CTG	TGC	CGC	TGT	GAT	GAC	GGT	GGC	TTC	ACC	TGC	CTG	CCG	CTG	TGC	AGT	336
	Leu	Cys	Arg	Cys	Asp	Asp	Gly	Gly	Phe	Thr	Cys	Leu	Pro	Leu	Cys	Ser	
				100				105					110				
60	GAG	GAT	GTG	CGG	CTG	CCC	AGC	TGG	GAC	TGC	CCA	CGC	CCC	AAG	AGA	ATA	384
	Glu	Asp	Val	Arg	Leu	Pro	Ser	Trp	Asp	Cys	Pro	Arg	Pro	Lys	Arg	Ile	
			115					120					125				

1. 1. The first  
 2. 2. The second  
 3. 3. The third  
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 6. 6. The sixth  
 7. 7. The seventh  
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 88. 88. The eighty-eighth  
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 93. 93. The ninety-third  
 94. 94. The ninety-fourth  
 95. 95. The ninety-fifth  
 96. 96. The ninety-sixth  
 97. 97. The ninety-seventh  
 98. 98. The ninety-eighth  
 99. 99. The ninety-ninth  
 100. 100. The hundredth

CAG GTG CCA GGA AAG TGC TGC CCC GAG TGG GTA TGT GAC CAG GGA GTG 432  
 Gln Val Pro Gly Lys Cys Cys Pro Glu Trp Val Cys Asp Gln Gly Val  
 130 135 140

5 ACA CCG GCG ATC CAG CGC TCC ACG GCG CAA GGA CAC CAA CTT TCT GCC 480  
 Thr Pro Ala Ile Gln Arg Ser Thr Ala Gln Gly His Gln Leu Ser Ala  
 145 150 155 160

10 CTT GTC ACT CCT GCC TCT GCT GAT GCT CCT TGT CCA AAT TGG AGC ACA 528  
 Leu Val Thr Pro Ala Ser Ala Asp Ala Pro Cys Pro Asn Trp Ser Thr  
 165 170 175

15 GCC TGG GGC CCC TGC TCA ACC ACC TGT GGG CTG GGC ATA GCC ACC CGA 576  
 Ala Trp Gly Pro Cys Ser Thr Thr Cys Gly Leu Gly Ile Ala Thr Arg  
 180 185 190

GTG TCC AAC CAG AAC CGA TTC TGC CAA CTG GAG ATC CAA CGC CGC CTG 624  
 Val Ser Asn Gln Asn Arg Phe Cys Gln Leu Glu Ile Gln Arg Arg Leu  
 195 200 205

20 TGT CTG CCC AGA CCC TGC CTG GCA GCC AGG AGC CAC AGC TCA TGG AAC 672  
 Cys Leu Pro Arg Pro Cys Leu Ala Ala Arg Ser His Ser Ser Trp Asn  
 210 215 220

25 AGT GCT TTC 681  
 Ser Ala Phe  
 225

30 (2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 227 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

40 Gln Leu Cys Arg Thr Pro Cys Thr Cys Pro Trp Thr Pro Pro Gln Cys  
 1 5 10 15

45 Pro Gln Gly Val Pro Leu Val Leu Asp Gly Cys Gly Cys Cys Lys Val  
 20 25 30

Cys Ala Arg Arg Leu Gly Glu Ser Cys Asp His Leu His Val Cys Asp  
 35 40 45

50 Pro Ser Gln Gly Leu Val Cys Gln Pro Gly Ala Gly Pro Gly Gly His  
 50 55 60

Gly Ala Val Cys Leu Leu Asp Glu Asp Asp Gly Ser Cys Glu Val Asn  
 65 70 75 80

55 Gly Arg Arg Tyr Leu Asp Gly Glu Thr Phe Lys Pro Asn Cys Arg Val  
 85 90 95

10010102103104105106107108109110111112113114115116117118119120121122123124125126127128129130131132133134135136137138139140141142143144145146147148149150151152153154155156157158159160161162163164165166167168169170171172173174175176177178179180181182183184185186187188189190191192193194195196197198199200201202203204205206207208209210211212213214215216217218219220221222223224225226227228229230231232233234235236237238239240241242243244245246247248249250251252253254255256257258259260261262263264265266267268269270271272273274275276277278279280281282283284285286287288289290291292293294295296297298299300301302303304305306307308309310311312313314315316317318319320321322323324325326327328329330331332333334335336337338339340341342343344345346347348349350351352353354355356357358359360361362363364365366367368369370371372373374375376377378379380381382383384385386387388389390391392393394395396397398399400401402403404405406407408409410411412413414415416417418419420421422423424425426427428429430431432433434435436437438439440441442443444445446447448449450451452453454455456457458459460461462463464465466467468469470471472473474475476477478479480481482483484485486487488489490491492493494495496497498499500501502503504505506507508509510511512513514515516517518519520521522523524525526527528529530531532533534535536537538539540541542543544545546547548549550551552553554555556557558559560561562563564565566567568569570571572573574575576577578579580581582583584585586587588589590591592593594595596597598599600601602603604605606607608609610611612613614615616617618619620621622623624625626627628629630631632633634635636637638639640641642643644645646647648649650651652653654655656657658659660661662663664665666667668669670671672673674675676677678679680681682683684685686687688689690691692693694695696697698699700701702703704705706707708709710711712713714715716717718719720721722723724725726727728729730731732733734735736737738739740741742743744745746747748749750751752753754755756757758759760761762763764765766767768769770771772773774775776777778779780781782783784785786787788789790791792793794795796797798799800801802803804805806807808809810811812813814815816817818819820821822823824825826827828829830831832833834835836837838839840841842843844845846847848849850851852853854855856857858859860861862863864865866867868869870871872873874875876877878879880881882883884885886887888889890891892893894895896897898899900901902903904905906907908909910911912913914915916917918919920921922923924925926927928929930931932933934935936937938939940941942943944945946947948949950951952953954955956957958959960961962963964965966967968969970971972973974975976977978979980981982983984985986987988989990991992993994995996997998999100010011002100310041005100610071008100910101011101210131014101510161017101810191020102110221023102410251026102710281029103010311032103310341035103610371038103910401041104210431044104510461047104810491050105110521053105410551056105710581059106010611062106310641065106610671068106910701071107210731074107510761077107810791080108110821083108410851086108710881089109010911092109310941095109610971098109911001101110211031104110511061107110811091110111111121113111411151116111711181119112011211122112311241125112611271128112911301131113211331134113511361137113811391140114111421143114411451146114711481149115011511152115311541155115611571158115911601161116211631164116511661167116811691170117111721173117411751176117711781179118011811182118311841185118611871188118911901191119211931194119511961197119811991200120112021203120412051206120712081209121012111212121312141215121612171218121912201221122212231224122512261227122812291230123112321233123412351236123712381239124012411242124312441245124612471248124912501251125212531254125512561257125812591260126112621263126412651266126712681269127012711272127312741275127612771278127912801281128212831284128512861287128812891290129112921293129412951296129712981299130013011302130313041305130613071308130913101311131213131314131513161317131813191320132113221323132413251326132713281329133013311332133313341335133613371338133913401341134213431344134513461347134813491350135113521353135413551356135713581359136013611362136313641365136613671368136913701371137213731374137513761377137813791380138113821383138413851386138713881389139013911392139313941395139613971398139914001401140214031404140514061407140814091410141114121413141414151416141714181419142014211422142314241425142614271428142914301431143214331434143514361437143814391440144114421443144414451446144714481449145014511452145314541455145614571458145914601461146214631464146514661467146814691470147114721473147414751476147714781479148014811482148314841485148614871488148914901491149214931494149514961497149814991500150115021503150415051506150715081509151015111512151315141515151615171518151915201521152215231524152515261527152815291530153115321533153415351536153715381539154015411542154315441545154615471548154915501551155215531554155515561557155815591560156115621563156415651566156715681569157015711572157315741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Leu Cys Arg Cys Asp Asp Gly Gly Phe Thr Cys Leu Pro Leu Cys Ser  
100 105 110

5 Glu Asp Val Arg Leu Pro Ser Trp Asp Cys Pro Arg Pro Lys Arg Ile  
115 120 125

Gln Val Pro Gly Lys Cys Cys Pro Glu Trp Val Cys Asp Gln Gly Val  
130 135 140

10 Thr Pro Ala Ile Gln Arg Ser Thr Ala Gln Gly His Gln Leu Ser Ala  
145 150 155 160

Leu Val Thr Pro Ala Ser Ala Asp Ala Pro Cys Pro Asn Trp Ser Thr  
15 165 170 175

Ala Trp Gly Pro Cys Ser Thr Thr Cys Gly Leu Gly Ile Ala Thr Arg  
180 185 190

20 Val Ser Asn Gln Asn Arg Phe Cys Gln Leu Glu Ile Gln Arg Arg Leu  
195 200 205

Cys Leu Pro Arg Pro Cys Leu Ala Ala Arg Ser His Ser Ser Trp Asn  
210 215 220

25 Ser Ala Phe  
225

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